AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph starting on page 18, line 14 as follows:

FIG. 3 shows the results of multiple alignment of the amino acid sequences of the inventive PAPP5 protein (SEQ ID NO: 16) and type 5 serine/threonine protein phosphatases isolated from several species.

H. sap PP5: *Homo sapiens* PP5 (GenBank accession No. CAA61595) (SEQ ID NO: 17);

M. mus PP5: *Mus musculus* PP5 (GenBank accession No. AAB70573) (SEQ ID NO: 18);

R. nor PP5: *Rattus norvegicus* PP5 (GenBank accession No. CAA54454) (SEQ ID NO: 19);

S. cer PP5: *Saccharomyces cerevisiae* PP5 (GenBank accession No. CAA58158) (SEQ ID NO: 20);

D. meg PP5: *Drosophila melanogaster* PP5 (GenBank accession No. CAB99478) (SEQ ID NO: 21); and

C. ele PP5: *Caenorhabditis elegans* PP5 (GenBank accession No. CAC51076) (SEQ ID NO: 22).

Please amend the paragraph starting on page 22, line 18 as follows:

Meanwhile, the results of PROSITE analysis revealed that TPR (tetratricopeptide repeat) which have been found in all PP5s by this time existed in the N-terminal region of the protein. Moreover, the C-terminal region of the protein contains a highly conserved type 2A serine/threonine protein phosphatase domain (PP2A), within which motifs (-GDXHGQ- [SEQ ID NO: 23], -GDXVXRG- [SEQ ID

NO: 24] and -RGNHE- [SEQ ID NO: 25]) necessary for the activity of serine/threonine phosphatase were included (see FIG. 3). The three conserved motifs play important roles in catalysis, substrate binding and metal ion binding (Ollendorff, V. *et al.*, *J. Biol. Chem.,* 272:32011-32018, 1998). In addition, the C-terminal region of the protein included consensus sequence "SAPNYC" (SEQ ID NO: 26) (Ollendorff, V. *et al.*, *J. Biol. Chem.,* 272:32011-32018, 1998) that binds to an okadaic acid, thereby inhibiting enzyme activity (see FIG. 3). From the above results, it could be found that the cDNA clone encodes a serine/threonine protein phosphatase.

Please amend the paragraph starting on page 32, line 10 as follows:

One mutant *papp5-1* was obtained from a separate T-DNA mutagenized population (SIGnAL T-DNA Express ~~(http://signal.salk.edu/cgi-bin/tdnaexpress)~~, Salk Institute Genomic Analysis Laboratory) prepared from Col-0 wild-type plants. The T-DNA in the mutant was found to be inserted into 1st intron (see FIG. 8A), and from this fact, *papp5-1* was assumed as a null allele. Another mutant *papp5-2* was isolated by screening DNAs isolated from a knock-out mutant population (Krysan, P. J., *et al.*, *Plant Cell,* 11:2283-2290, 1999) prepared from Ws-2 wild-type plants. The T-DNA in *papp5-2* was found to be inserted into 12nd intron (see FIG. 8A).

Please amend the paragraph starting on page 39, line 12 as follows:

A reverse genetic approach for dominant negative mutation was used to investigate the roles of TPR domain of PAPP5. The TPR domain-coding region (the sequence of amino acids 1-138 of SEQ ID NO: 4) was amplified by PCR using

primers set forth in SEQ ID NO: 5 and SEQ ID NO: 10. The PCR reaction consisted of predenaturation of template DNA for 5 min at 94 °C, and then, 30 cycles of 30 sec at 94 °C, 30 sec at 50 °C and 1 min at 72 °C, followed by 10 min at 72 °C. Thereafter, the PCR product was cloned into a pNB96 vector (see FIG. 12A). The prepared vector was named "pNB96-TPR". The pNB96-TPR vector was introduced into *Agrobacterium* strain AGL1 by electroporation. Next, according to the floral-dip method (SIGnAL T-DNA Express ~~(http://signal.salk.edu/cgi-bin/tdnaexpress)~~, Salk Institute Genomic Analysis Laboratory), *Arabidopsis thaliana* was transformed with the transformed *Agrobacterium*. 25 μg/μl of DL-PPT (Duchefa Biochemie BV) was used to select transgenic plants. Total 25 T1 lines were obtained and named "PAPP5-DN". Thereafter, on the basis of segregation of DL-PPT resistance, homozygous T3 seeds were isolated. The T3 plants were grown in the white light condition, and the resulting plants have shorter height, multiple shoots, and dwarfing of the floral shoot internodes, as compared to wild-type plants (see FIG. 12B). This is thought to be induced by improved protein-protein interaction, in view of the fact that the TPR domain of PAPP5 is involved in protein-protein interaction. Furthermore, this indicates that the introduction and overexpresison of the TPR domain of PAPP5 in plants can introduce dwarf characteristics into the plants.

In compliance with 37 C.F.R. § 1.823(a), please insert the attached substitute paper copy of the "Sequence Listing" after the last page of the above-identified application to replace the Sequence Listing previously filed on August 24, 2006.